

受付番号は、【20090106184136\_3410】です。

\*\*\*\*\* [align] \*\*\*\*\*

options = -align -gapdist=8 -maxdiv=40

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQIDNO\_1 881 bp

Sequence 2: BQ671560 889 bp

Sequence 3: BQ672221 979 bp

Sequence 4: BI914593 735 bp

Start of Pairwise alignments

Aligning...

== Aligned score is not displayed ==

Start of Multiple Alignment

There are 3 groups

Aligning...

== Aligned score is not displayed ==

Alignment Score 33195

query.aln

CLUSTAL W (1.83) multiple sequence alignment

```
SEQIDNO_1  -----GGGCCATGACCCCGCTGCTCTGTCTTGCAGGCTCGTC
BI914593
BQ672221  CGCGGCTGCCCGAGCGCGCGGCCATGACCCCGCTGCTCTGTCTTGCAGGCTCGTC
BQ671560  CGCGGCTGCCCGAGCGCGCGGCCATGACCCCGCTGCTCTGTCTTGCAGGCTCGTC
```

```
SEQIDNO_1  GCGCGGGCCCCCGAGCCGACCGCGCGGCCACCACCAGCGCCGGCGGGCCTCG
BI914593
BQ672221  GCGCGGGCCCCCGAGCCGACCGCGCGGCCACCACCAGCGCCGGCGGGCCTCG
BQ671560  GCGCGGGCCCCCGAGCCGACCGCGCGGCCACCACCAGCGCCGGCGGGCCTCG
```

```
SEQIDNO_1  CGCGCCTCGGGCGCGGCTCCGCAGTGAGCCACCAAGAAGGAAGCGGCCTGCAGAGGTGC
BI914593  -----GCAGTGAGCCACCAAGAAGGAAGCGGCCTGCAGAGGTGC
BQ672221  CGCGCCTCGGGCGCGGCTCCGCAGTGAGCCACCAAGAAGGAAGCGGCCTGCAGAGGTGC
BQ671560  CGCGCCTCGGGCGCGGCTCCGCAGTGAGCCACCAAGAAGGAAGCGGCCTGCAGAGGTGC
```

\*\*\*\*\*

```
SEQIDNO_1  CGACATGGGGCTTAAGATGTCCTGCCTGAAAGGCTTTCAAATGTGTGTCAGCAGCAGCAG
BI914593  CGACATGGGGCTTAAGATGTCCTGCCTGAAATGC-----AGCAG
BQ672221  CGACATGGGGCTTAAGATGTCCTGCCTGAAAGGCTTTCAAATGTGTGTCAGCAGCAGCAG
BQ671560  CGACATGGGGCTTAAGATGTCCTGCCTGAAAGGCTTTCAAATGTGTGTCAGCAGCAGCAG
```

\*\*\*\*\* \*\*

\*\*\*\*\*

```
SEQIDNO_1  CAGCAGCCACGACGAGGCCCGCTCCTGAACGACAAGCACCTGGACGTGCCCGACATCAT
BI914593  CAGCAGCCACGACGAGGCCCGCTCCTGAACGACAAGCACCTGGACGTGCCCGACATCAT
BQ672221  CAGCAGCCACGACGAGGCCCGCTCCTGAACGACAAGCACCTGGACGTGCCCGACATCAT
```

BQ671560 CAGCAGCCACGACGAGGCCCGCTCCTGAACGACAAGCACCTGGACGTGCCGACATCAT  
 \*\*\*\*\*  
 SEQIDNO\_1 CATCAGCCCCCACCACGAGGCGATGATGCTGCCGAGGGACTTGGGAGCACAGTCTG  
 BI914593 CATCAGCCCCCACCACGAGGCGATGATGCTGCCGAGGGACTTGGGAGCACAGTCTG  
 BQ672221 CATCAGCCCCCACCACGAGGCGATGATGCTGCCGAGGGACTTGGGAGCACAGTCTG  
 BQ671560 CATCAGCCCCCACCACGAGGCGATGATGCTGCCGAGGGACTTGGGAGCACAGTCTG  
 \*\*\*\*\*  
 SEQIDNO\_1 GCTGGATGAGACAGGTCGTGCCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGG  
 BI914593 GCTGGATGAGACAGGTCGTGCCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGG  
 BQ672221 GCTGGATGAGACAGGTCGTGCCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGG  
 BQ671560 GCTGGATGAGACAGGTCGTGCCAGATGATGGAGAAATCGACCCAGAAGCCTGAGGAGG  
 \*\*\*\*\*  
 SEQIDNO\_1 TGTCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGC  
 BI914593 TGTCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGC  
 BQ672221 TGTCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGC  
 BQ671560 TGTCTGGGTTTGGCTGGCTGGCTCCTGCTCCAGCGGCCCGGCTTCAGGTGTCCGGGGGC  
 \*\*\*\*\*  
 SEQIDNO\_1 GTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAACAGCGAACCC-GGGCC  
 BI914593 GTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAACAGCGAACCC-GGGCC  
 BQ672221 GTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAACAGCGAACCCGGGCC  
 BQ671560 GTGGCTGCCTGGAGCAGGTGTGCTGAATACCCTGGATGGGAACAGCGAACCC-GGGCC  
 \*\*\*\*\*  
 SEQIDNO\_1 TCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCAC-TTCCAGAACA  
 BI914593 TCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCAC-TTCCAGAACA  
 BQ672221 TCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCACCTTCCAGAACA  
 BQ671560 TCCGCTCAGAGAGACGTGGCAGGACCAGCGAGGAATCCAGCCTGTCCAC-TTCCAGAACA  
 \*\*\*\*\*  
 SEQIDNO\_1 GTGTTTCCAGGCCCC-GCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGTGAC  
 BI914593 GTGTTTCCAGGCCCC-GCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGTGAC  
 BQ672221 GTGTTTCCAGGCCCC-GCTGAGTGGACCGGACCTCTGACACCTCCAGGTTCTTGTGAC  
 BQ671560 GTGTTTCCAGGCCCCCGCTGAGGGGACCGGACCTCTGACACCTCCCGTTCTTGTGAC  
 \*\*\*\*\*  
 SEQIDNO\_1 TCCGGCCTGGTGAAGGGAGCGCCATGGTCC-TGGCTGTTGGGGT-CCCAGGGAGAGGCT  
 BI914593 TCCGGCCTGGTGAAGGGAGCGCCATGGTCC-TGGCTGTTGGGGT-CCCAGGCAGAGGCT  
 BQ672221 TCCGGCCTGNTGAAGGGAGCGCCATGGTCC-TGGCTGGTGGGGT-CCCAGGGAGAGGCT  
 BQ671560 TCCGGCCTGGGGAAAGGGAACCGCTTGGTCCCTGGCTGTTGGGGGGCCAGGGAAGGGT  
 \*\*\*\*\*  
 SEQIDNO\_1 CTC-TTCTGGACAAACACACCCTCCAGCCCCC-AGGGCTGTGCA-AACACATGCCCCTG  
 BI914593 CTC-TTCTGGACAAACACACCCTCCAGCCCCCAGGGCTGTGCA-AACACATGCCCCTC  
 BQ672221 CTCCTTCTGGACAAACACACCCTTCCAGCCCCCAGGGCTGTGCA-AACACATGCCCCCG  
 BQ671560 CGTCTTCGAGCAAACGAACCTTTGAAAGCCCCCGGGCATGGACAAACAAGCCCCG  
 \* \*\* \* \* \* \* \*  
 SEQIDNO\_1 ----CCATAAGCACCAACAAGAACTTCTT----GCAGGTGGAGTGGCTGTTTTTATAAGTT--  
 BI914593 ----CCATAAGCACCAACAAGAACTTCTT----GCAGGTGGAGTGGCTGTATTTTATAAGTT--  
 BQ672221 G----CCATAAGCCCCACAAAAACCTTCTTGCCGGGGGAAGGGCTTTTTTTTTTAAACC  
 BQ671560 GTCCATAGGACCCAGGAAGAAAGTTCTTGGAGGCCGGGCGGGAATGCGGCTGTACC--  
 \* \* \* \* \*  
 SEQIDNO\_1 ----GTTTTACAGA----TACGGAAACAGTCCAAATGGGA----TTTATAATTTCTTTTTTG  
 BI914593 ----GTTTTACAGA----TACGGAAACAGTCCAAATGGGA----TTTATAATTTCTTTTTTG  
 BQ672221 CGCGTTTTACGAGTGCAGGACACCCCATACCGGGACTTTATCACTTCTACTTG  
 BQ671560 -----TACCAAGCTTACAGACTCGGCGGAAAAAGGA-----CGGCGCAAGGCCG  
 \*\*\* \* \* \* \* \*

```

SEQIDNO_1      CATTATAAATAA----AGATCCTCTGTAAC-----
BI914593       CATTATAAATAA----AGATCC-----
BQ672221       CGCCATGATCGAGGCGAGGTCCTGTTGCGTGCCCGCCGCACACAGGCTCGCCCCCGT
BQ671560       CGCCGG-----
*
```

```

SEQIDNO_1      -----
BI914593       -----
BQ672221       ACCATCCGCGGATCGCCGGGCACCG
BQ671560       -----
```

```

query.dnd
(
  SEQIDNO_1:-0.00673,
  (
    BQ671560:0.09278,
    BQ672221:0.04332)
  :0.06807,
  BI914593:0.01353);
```

\*\*\*\*\* [tree] \*\*\*\*\*

options = -tree -kimura -tossgaps

CLUSTAL W (1.83) Multiple Sequence Alignments

```

Sequence format is Clustal
Sequence 1: SEQIDNO_1      985 bp
Sequence 2: BI914593      985 bp
Sequence 3: BQ672221      985 bp
Sequence 4: BQ671560      985 bp
```

```

query.ph
(
  (
    SEQIDNO_1:-0.00039,
    BI914593:0.00602)
  :0.03370,
  BQ672221:0.02953,
  BQ671560:0.11040);
```